Amendments to the Claims

The current status of the claims is as follows:

Claims 1-38 (Canceled)

39. (Previously Presented) A kit for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22); and

a second oligonucleotide comprising the nucleotide base sequence of xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2),

wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein each said oligonucleotide is from 22 to 100 bases in length.

40. (Previously Presented) An oligonucleotide for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said oligonucleotide being from 22 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22) or a sequence of the same length and fully complementary thereto, wherein x is nothing or is a sequence recognized by an RNA polymerase.

41. (Previously Presented) A kit for use in amplifying and detecting *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide of from 24 to 100 nucleotide bases in length and comprising the nucleotide base sequence of SEQ ID NO: 3; and

a second oligonucleotide of from 22 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22) or

xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase.

42. (Previously Presented) A kit for use in amplifying and detecting *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide of from 23 to 100 nucleotide bases in length and comprising the nucleotide base sequence of SEQ ID NO: 8; and

a second oligonucleotide of from 20 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

Claims 43-47 (Canceled)

48. (Previously Presented) The kit of claim 41, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

49. (Previously Presented) The kit of claim 48 further comprising a third oligonucleotide having a 3' end which is unmodified, wherein said third oligonucleotide is from 20 to 100 nucleotide bases in length and comprises the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein the nucleotide base sequences of said second and third oligonucleotides are different.

50. (Previously Presented) The oligonucleotide of claim 40, wherein said oligonucleotide has a 3' end which is modified to reduce or block extension of said oligonucleotide by a polymerase.

51. (Previously Presented) A composition comprising:

a first oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said first oligonucleotide has a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

52. (Canceled)

53. (Canceled)

54. (Previously Presented) The composition of claim 51 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension by a polymerase, wherein the 3' ends of said second and third oligonucleotides are differently modified.

55. (Previously Presented) The kit of claim 42, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

56. (Previously Presented) The kit of claim 55 further comprising a third oligonucleotide having a 3' end which is not modified to reduce or block extension of said third oligonucleotide by a polymerase.

Claims 57-66 (Canceled)

67. (Previously Presented) A primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

68. (Previously Presented) The primer oligonucleotide of claim 67, said primer being from 15 to 50 nucleotide bases in length.

69. (Previously Presented) The primer oligonucleotide of claim 67, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

70. (Previously Presented) The primer oligonucleotide of claim 67, wherein the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region and, optionally, a sequence recognized by an RNA polymerase.

71. (Previously Presented) The primer oligonucleotide of claim 67 further comprising a sequence recognized by an RNA polymerase.

72. (Previously Presented) The primer oligonucleotide of claim 71, said primer oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 1.

73. (Previously Presented) The primer oligonucleotide of claim 71, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 1.

74. (Canceled)

75. (Previously Presented) A composition for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said composition comprising:

a first primer oligonucleotide consisting of an oligonucleotide up to 100 nucleotide bases in length which hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO:23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said first primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region; and

a second primer oligonucleotide consisting of an oligonucleotide up to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 7, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

76. (Canceled)

77. (Canceled)

78. (Previously Presented) The composition of claim 75, wherein at least one of said first and second primer oligonucleotides further comprises a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

79. (Previously Presented) The composition of claim 75 further comprising a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a third nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein the nucleotide base sequence of said third region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

80. (Previously Presented) The composition of claim 79, wherein said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said third region.

81. (Canceled)

82. (Previously Presented) The composition of claim 79, wherein said probe further comprises a detectable label.

83. (Previously Presented) The composition of claim 82, wherein said detectable label is an acridinium ester.

84. (Previously Presented) A composition for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said composition comprising first and second primer oligonucleotides, each of said primer oligonucleotides being up to 100 nucleotide bases in length,

wherein said first primer oligonucleotide hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said first primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region, and

wherein said second primer oligonucleotide hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

85. (Canceled)

86. (Previously Presented) The composition of claim 84, wherein:

said first primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

wherein said second primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

87. (Canceled)

88. (Previously Presented) The composition of claim 84 or 86, wherein at least one of said first and second primer oligonucleotides further comprises a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

89. (Previously Presented) The composition of claim 84 or 86 further comprising a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a third nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein the nucleotide base sequence of said third region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

90. (Previously Presented) The composition of claim 89, wherein:

said first primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region;

said second primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region; and

said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said third region.

91. (Canceled)

92. (Previously Presented) The composition of claim 89, wherein said probe comprises a detectable label.

93. (Previously Presented) The composition of claim 92 wherein said detectable label is an acridinium ester.

94. (Canceled)

95. (Previously Presented) A helper probe consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:5.

96. (Previously Presented) A probe mix comprising:

a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

a helper oligonucleotide consisting essentially of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9 and SEQ ID NO: 10.

97. (Canceled)

98. (Currently Amended) A probe mix comprising:

a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

a helper oligonucleotide consisting essentially of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 4 and SEQ ID NO: 5.

99. (Canceled)

100. (Previously Presented) A kit for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23); and

a second oligonucleotide comprising the nucleotide base sequence of xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7),

wherein x is nothing or is a sequence recognized by an RNA polymerase.

101. (Previously Presented) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3 and SEQ ID NO: 8, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 22 and SEQ ID NO: 23, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

102. (Previously Presented) A composition comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3' end of a (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second primer sequence, if present, is different than said modification to said first primer sequence;

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification;

an enzyme selected from the group consisting of a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequence of said first and second oligonucleotides.

103. (Previously Presented) The composition of claim 102, wherein said (+) target sequence is RNA.

104. (Previously Presented) The composition of claim 102, wherein said composition further comprises RNAse H activity.

105. (Previously Presented) The composition of claim 104, wherein said RNAse H activity is supplied by an exogenous RNAse H from *E. coli.*

106. (Previously Presented) The composition of claim 104, wherein said RNAse H activity is supplied by a reverse transcriptase.

107. (Previously Presented) The composition of claim 102, wherein said enzyme is a reverse transcriptase which is both a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase.

108. (Previously Presented) The composition of claim 102 further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

109. (Previously Presented) The composition of claim 102 further comprising a helper oligonucleotide.

110. (Previously Presented) The composition of claim 102, wherein said first and said second oligonucleotides are present in a molar ratio of between 1:1 and 1000:1.

111. (Previously Presented) The composition of claim 102, wherein said second primer sequence comprises said modification at or near its 3' end.

112. (Previously Presented) The composition of claim 111 further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said first and second oligonucleotides and an optionally present 5' promoter sequence,

wherein said fourth primer sequence does not contain a modification at or near its 3' end which reduces or blocks extension of said fourth primer sequence.

113. (Previously Presented) The composition of claim 111, wherein the 3' end modifications to said first and second primer sequences are independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

114. (Previously Presented) The composition of claim 111, wherein the 3' end modifications to said first and second primer sequences are independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

115. (Previously Presented) The composition of claim 102, wherein said third primer sequence does not comprise said modification at or near its 3' end.

116. (Previously Presented) The composition of claim 102, wherein said third oligonucleotide comprises said 5' promoter sequence.

117. (Previously Presented) The composition of claim 116, wherein said third primer sequence comprises said modification at or near its 3' end.

118. (Previously Presented) The composition of claim 102, wherein said first and second primer sequences are the same.

119. (Previously Presented) The composition of claim 102, wherein said first and second primer sequences are different.

120. (Previously Presented) A composition comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3' end of a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification;

a third oligonucleotide comprising a third primer sequence able to hybridize at or near the 3' end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide, and wherein said modification to said third oligonucleotide, if present, is different than said modification to said second oligonucleotide;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

121. (Previously Presented) The composition of claim 120, wherein said (+) target sequences RNA.

122. (Previously Presented) The composition of claim 120, wherein said composition further comprises RNAse H activity.

123. (Previously Presented) The composition of claim 122, wherein said RNAse H activity is supplied by an exogenous RNAse H from *E. coli.*

124. (Previously Presented) The composition of claim 122, wherein said RNAse H activity is supplied by a reverse transcriptase.

125. (Previously Presented) The composition of claim 120, wherein said enzyme is a reverse transcriptase which is both a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase.

126. (Previously Presented) The composition of claim 120 further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

127. (Previously Presented) The composition of claim 120 further comprising a helper oligonucleotide.

128. (Previously Presented) The composition of claim 120, wherein said second and said third oligonucleotides are present in a molar ratio of between 1:1 and 1000:1.

129. (Previously Presented) The composition of claim 120, wherein said third primer sequence comprises said modification at its 3' end.

130. (Previously Presented) The composition of claim 129 further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said second and third oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth primer sequence does not comprise a modification at or near its 3' end which reduces or blocks primer extension of said fourth primer sequence.

131. (Previously Presented) The composition of claim 129, wherein said 3' end modifications to said second and third primer sequences are independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

132. (Previously Presented) The composition of claim 129, wherein the 3' end modifications to said second and third primer sequences are independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

133. (Previously Presented) The composition of claim 120, wherein said first primer sequence does not comprise said modification at or near its 3' end.

134. (Previously Presented) The composition of claim 120, wherein said first oligonucleotide comprises said 5' promoter sequence.

135. (Previously Presented) The composition of claim 120, wherein said first primer sequence comprises said modification at or near its 3' end.

136. (Previously Presented) The composition of claim 134, wherein said promoter sequences of said first, second and third oligonucleotides are the same.

137. (Previously Presented) The composition of claim 120, wherein said promoter sequences of said second and third primer sequences are the same.

138. (Previously Presented) The composition of claim 120, wherein said promoter sequences of said second and said third primer sequences are different.

139. (Previously Presented) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3' end of a (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second primer sequence, if present, is different than said modification to said first primer sequence;

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

140. (Previously Presented) The kit of claim 139 further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

141. (Previously Presented) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3' end of a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification;

a third oligonucleotide comprising a third primer sequence able to hybridize at or near the 3' end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide and said modification to said third oligonucleotide, if present, is different than said modification to said second oligonucleotide;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

142. (Previously Presented) The kit of claim 141 further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

143. (Previously Presented) An oligonucleotide for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said oligonucleotide being from 20 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or a sequence of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

144. (Previously Presented) The composition of claim 143, wherein said oligonucleotide has a 3' end which is modified to reduce or block extension of said oligonucleotide by a polymerase.

145. (Previously Presented) A composition comprising:

a first oligonucleotide having a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide having a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase, wherein each of said first and second oligonucleotides comprises a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23), xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), and sequences of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

146. (Previously Presented) The composition of claim 145 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension of said third oligonucleotide by a polymerase, wherein the 3' ends of said second and third oligonucleotides are differently modified.

147. (Previously Presented) A primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

148. (Previously Presented) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide is from 15 to 50 nucleotide bases in length.

149. (Previously Presented) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide is from 20 to 100 nucleotide bases in length.

150. (Previously Presented) The primer oligonucleotide of claim 69, wherein said primer oligonucleotide is from 22 to 100 nucleotide bases in length.

151. (Previously Presented) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

152. (Previously Presented) The primer oligonucleotide of claim 147, wherein the nucleotide base sequence of said primer oligonucleotide is of the same length and fully complementary to the nucleotide base sequence of said region and, optionally, a sequence recognized by an RNA polymerase.

153. (Previously Presented) The primer oligonucleotide of claim 147 further comprising a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

154. (Previously Presented) The primer oligonucleotide of claim 153, wherein said primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 6 or SEQ ID NO: 19.

155. (Previously Presented) The primer oligonucleotide of claim 153, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 6 or SEQ ID NO: 19.

156. (Previously Presented) The composition of claim 82 further comprising:

a first helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 9; and

a second helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 10.

157. (Previously Presented) The composition of claim 101 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

158. (Previously Presented) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22 and SEQ ID NO: 23, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto, and wherein said oligonucleotide primer includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

159. (Canceled)

160. (Previously Presented) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting the nucleotide base sequences of SEQ ID NO: 22 and SEQ ID NO: 2, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

161. (Previously Presented) The composition of claim 160 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4 and SEQ ID NO: 5, and sequences of the same length and fully complementary thereto.

162. (Previously Presented) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region.

163. (Canceled)

164. (Previously Presented) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said

second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23 and SEQ ID NO: 7, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

165. (Previously Presented) The composition of claim 164 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting the nucleotide base sequences of SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

166. (Previously Presented) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

167. (Previously Presented) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence of the same length and fully complementary thereto, and a hybridization probe at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said probe hybridizes with specificity to said region, or a sequence of the same length and fully complementary thereto, and wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

168. (Previously Presented) The kit of claim 41 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4 and SEQ ID NO: 5, and sequences of the same length and fully complementary thereto.

169. (Previously Presented) The kit of claim 42 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

170. (Previously Presented) The composition of claim 80, wherein said probe further comprises a detectable label.

171. (Previously Presented) The composition of claim 170, wherein said detectable label is an acridinium ester.

172. (Previously Presented) The composition of claim 170 further comprising:

a first helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 9; and

a second helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 10.

173. (Previously Presented) The kit of claim 162 further comprising a second primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, the RNA equivalent thereof,

and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

174. (Previously Presented) The kit of claim 166, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 23 or a sequence of the same length and fully complementary thereto.

175. (Canceled)

176. (Canceled)

177. (Previously Presented) A hybridization probe at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said probe hybridizes with specificity to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

178. (Previously Presented) An oligonucleotide at least 20 bases in length, wherein the nucleotide base sequence of said oligonucleotide consists of or is contained within the nucleotide base sequence xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7) or a sequence of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

179. (Previously Presented) A kit comprising a primer oligonucleotide at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said primer hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group of nucleotide base sequences of SEQ ID NO: 7, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

180. (Previously Presented) The kit of claim 39, wherein each of said first and second oligonucleotides is up to 60 nucleotide bases in length.

181. (Previously Presented) The kit of claim 39, wherein:

the nucleotide base sequence of said first oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 22 and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said second oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 2 and, optionally, a sequence recognized by an RNA polymerase.

182. (Previously Presented) The oligonucleotide of claim 40, wherein said oligonucleotide is up to 60 nucleotide bases in length.

183. (Previously Presented) The oligonucleotide of claim 40, wherein the nucleotide base sequence of said oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 22 and, optionally, a sequence recognized by an RNA polymerase.

184. (Previously Presented) The kit of claim 41, wherein:

the nucleotide base sequence of said first oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 3; and

the nucleotide base sequence of said second oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 22 or SEQ ID NO: 2 and, optionally, a sequence recognized by an RNA polymerase.

185. (Previously Presented) The kit of claim 42, wherein:

the nucleotide base sequence of said first oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 8; and

the nucleotide base sequence of said second oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 23 or SEQ ID NO: 7 and, optionally, a sequence recognized by an RNA polymerase.

186. (Previously Presented) The primer oligonucleotide of claim 73, wherein the nucleotide base sequence of said primer oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 1.

187. (Previously Presented) The composition of claim 75, wherein each of said first and second primer oligonucleotides is up to 60 nucleotide bases in length.

188. (Previously Presented) The composition of claim 75, wherein:

said first primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

said second primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

189. (Previously Presented) The composition of claim 75, wherein:

the nucleotide base sequence of said first primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said second primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

190. (Previously Presented) The composition of claim 79, wherein:

said first primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region;

said second primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region; and

said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said third region.

191. (Previously Presented) The composition of claim 79, wherein:

the nucleotide base sequence of said first primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, a sequence recognized by an RNA polymerase;

the nucleotide base sequence of said second primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said probe consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said third region.

192. (Previously Presented) The composition of claim 84, wherein each of said first and second primer oligonucleotides is up to 60 nucleotide bases in length.

193. (Previously Presented) The composition of claim 84, wherein:

the nucleotide base sequence of said first primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said second primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

194. (Previously Presented) The composition of claim 89, wherein:

the nucleotide base sequence of said first primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, a sequence recognized by an RNA polymerase;

the nucleotide base sequence of said second primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said probe consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said third region.

195. (Previously Presented) The probe mix of claim 96, wherein said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

196. (Previously Presented) The probe mix of claim 96, wherein the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said region.

197. (Previously Presented) The probe mix of claim 98, wherein said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

198. (Previously Presented) The probe mix of claim 98, wherein the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said region.

199. (Previously Presented) The kit of claim 100, wherein:

the nucleotide base sequence of said first oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 23 and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said second oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 7 and, optionally, a sequence recognized by an RNA polymerase.

200. (Previously Presented) The composition of claim 101, wherein:

said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

201. (Previously Presented) The composition of claim 101, wherein:

the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said first region; and

the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

202. (Previously Presented) The oligonucleotide of claim 143, wherein said oligonucleotide is up to 60 nucleotide bases in length.

203. (Previously Presented) The composition of claim 143, wherein the nucleotide base sequence of said oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 23 and, optionally, a sequence recognized by an RNA polymerase.

204. (Previously Presented) The kit of claim 158, wherein said primer oligonucleotide is up to 60 nucleotide bases in length.

205. (Previously Presented) The kit of claim 158, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

206. (Previously Presented) The kit of claim 158, wherein the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region and, optionally, a sequence recognized by an RNA polymerase.

207. (Canceled)

208. (Canceled)

209. (Previously Presented) The composition of claim 160, wherein:

said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

210. (Previously Presented) The composition of claim 160, wherein:

the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said first region; and

the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

211. (Previously Presented) The kit of claim 162, wherein said primer oligonucleotide is up to 60 nucleotide bases in length.

212. (Previously Presented) The kit of claim 162, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region.

213. (Previously Presented) The kit of claim 162, wherein the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, as sequence recognized by an RNA polymerase.

214. (Canceled)

215. (Canceled)

216. (Previously Presented) The composition of claim 164, wherein:

said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

217. (Previously Presented) The composition of claim 164, wherein:

the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said first region; and

the nucleotide base sequence of said primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

218. (Previously Presented) The kit of claim 166, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

219. (Previously Presented) The kit of claim 166, wherein the nucleotide base sequence of said primer oligonucleotide consists a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region and, optionally, a sequence recognized by an RNA polymerase.

220. (Previously Presented) The composition of claim 167, wherein said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

221. (Previously Presented) The composition of claim 167, wherein the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said region.

222. (Previously Presented) The kit of claim 173, wherein each of said first and second primer oligonucleotides is up to 60 nucleotide bases in length.

223. (Previously Presented) The kit of claim 173, wherein:

said first primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region; and

said second primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region.

224. (Previously Presented) The kit of claim 173, wherein:

the nucleotide base sequence of said first primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said first region and, optionally, a sequence recognized by an RNA polymerase; and

the nucleotide base sequence of said second primer oligonucleotide consists of a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said second region and, optionally, a sequence recognized by an RNA polymerase.

225. (Canceled)

226. (Canceled)

227. (Previously Presented) The probe of claim 177, wherein said probe comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

228. (Previously Presented) The probe of claim 177, wherein the nucleotide base sequence of said probe is of the same length and fully complementary to the nucleotide base sequence of said region.

229. (Previously Presented) The oligonucleotide of claim 178, wherein the nucleotide base sequence of said oligonucleotide consists of the nucleotide base sequence of SEQ ID NO: 7.

230. (Previously Presented) The kit of claim 179, wherein said primer oligonucleotide comprises a nucleotide base sequence of the same length and fully complementary to the nucleotide base sequence of said region.

231. (Previously Presented) The kit of claim 179, wherein the nucleotide base sequence of said primer oligonucleotide is of the same length and fully complementary to the nucleotide base sequence of said region and, optionally, a sequence recognized by an RNA polymerase.